

Automated Docking Screens: A Feasibility Study

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Molecular Docking Screens Using Comparative Models of Proteins. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 2512-2527.	5.4	132
2	The Drug Discovery Portal: A Computational Platform for Identifying Drug Leads from Academia. <i>Current Pharmaceutical Design</i> , 2010, 16, 1697-1702.	1.9	3
3	Structure-Based Approaches to Target Fishing and Ligand Profiling. <i>Molecular Informatics</i> , 2010, 29, 176-187.	2.5	132
4	A Structure-Based Approach for Mapping Adverse Drug Reactions to the Perturbation of Underlying Biological Pathways. <i>PLoS ONE</i> , 2010, 5, e12063.	2.5	47
5	e-LEA3D: a computational-aided drug design web server. <i>Nucleic Acids Research</i> , 2010, 38, W615-W621.	14.5	107
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18	Reactome: a database of reactions, pathways and biological processes. <i>Nucleic Acids Research</i> , 2011, 39, D691-D697.	14.5	1,391

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